

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/581,570
Source: IFWP
Date Processed by STIC: 6/14/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 06/14/2006

PATENT APPLICATION: US/10/581,570

TIME: 10:12:07

Input Set : A:\seq listing.app

Output Set: N:\CRF4\06142006\J581570.raw

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3 <110> APPLICANT: Liao et al.
5 <120> TITLE OF INVENTION: PRODUCTION OF 3-HYDROXYPROPIONIC ACID USING BETA
6   -ALANINE/PYRUVATE AMINOTRANSFERASE
8 <130> FILE REFERENCE: 66576-05
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/581,570
C--> 10 <141> CURRENT FILING DATE: 2006-06-02
10 <150> PRIOR APPLICATION NUMBER: PCT/US2004/040827
11 <151> PRIOR FILING DATE: 2004-12-06
13 <150> PRIOR APPLICATION NUMBER: US 60/527,357
14 <151> PRIOR FILING DATE: 2003-12-04
16 <160> NUMBER OF SEQ ID NOS: 28
18 <170> SOFTWARE: PatentIn version 3.2
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 60
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial
25 <220> FEATURE:
26 <223> OTHER INFORMATION: PCR primer
28 <400> SEQUENCE: 1
29 atatttttag tagcttaa atgtgattcaac atcactggag gtgtaggctg gagctgcttc 60
32 <210> SEQ ID NO: 2
33 <211> LENGTH: 60
34 <212> TYPE: DNA
35 <213> ORGANISM: Artificial
37 <220> FEATURE:
38 <223> OTHER INFORMATION: PCR primer
40 <400> SEQUENCE: 2
41 tatctgaatc agctcccctg gaatgcaggg gagcggcaag catatgaata tcctccttag 60
44 <210> SEQ ID NO: 3
45 <211> LENGTH: 22
46 <212> TYPE: DNA
47 <213> ORGANISM: Artificial
49 <220> FEATURE:
50 <223> OTHER INFORMATION: PCR primer
52 <400> SEQUENCE: 3
53 ttcaatatcg ccatagcttt ca 22
56 <210> SEQ ID NO: 4
57 <211> LENGTH: 19
58 <212> TYPE: DNA
59 <213> ORGANISM: Artificial
61 <220> FEATURE:
62 <223> OTHER INFORMATION: PCR primer
64 <400> SEQUENCE: 4

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65 gaggatgaaa ggtcattgg 19
68 <210> SEQ ID NO: 5
69 <211> LENGTH: 33
70 <212> TYPE: DNA
71 <213> ORGANISM: Artificial
73 <220> FEATURE:
74 <223> OTHER INFORMATION: PCR primer
76 <400> SEQUENCE: 5
77 aagcccgagg atcgacatat gaaccagccg etc 33
80 <210> SEQ ID NO: 6
81 <211> LENGTH: 22
82 <212> TYPE: DNA
83 <213> ORGANISM: Artificial
85 <220> FEATURE:
86 <223> OTHER INFORMATION: PCR primer
88 <400> SEQUENCE: 6
89 ccacctgcac ggtgggtacg gc 22
92 <210> SEQ ID NO: 7
93 <211> LENGTH: 35
94 <212> TYPE: DNA
95 <213> ORGANISM: Artificial
97 <220> FEATURE:
98 <223> OTHER INFORMATION: PCR primer
100 <400> SEQUENCE: 7
101 tcttccgagg aaccgcatat gaacatgccc gaaac 35
104 <210> SEQ ID NO: 8
105 <211> LENGTH: 41
106 <212> TYPE: DNA
107 <213> ORGANISM: Artificial
109 <220> FEATURE:
110 <223> OTHER INFORMATION: PCR primer
112 <400> SEQUENCE: 8
113 gcatacgcct ggcattaatt aaggaaagat cagtcgatca g 41
116 <210> SEQ ID NO: 9
117 <211> LENGTH: 27
118 <212> TYPE: DNA
119 <213> ORGANISM: Artificial
121 <220> FEATURE:
122 <223> OTHER INFORMATION: PCR primer
124 <400> SEQUENCE: 9
125 atacatatga ccgacatcgc attcctc 27
128 <210> SEQ ID NO: 10
129 <211> LENGTH: 28
130 <212> TYPE: DNA
131 <213> ORGANISM: Artificial
133 <220> FEATURE:
134 <223> OTHER INFORMATION: PCR primer
136 <400> SEQUENCE: 10
137 atagtcgact tagggatgaa gcagtggag 28

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Input Set : A:\seq_listing.app

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140 <210> SEQ ID NO: 11
141 <211> LENGTH: 64
142 <212> TYPE: DNA
143 <213> ORGANISM: Artificial
145 <220> FEATURE:
146 <223> OTHER INFORMATION: PCR primer
149 <220> FEATURE:
150 <221> NAME/KEY: misc_feature
151 <222> LOCATION: (46)..(46)
152 <223> OTHER INFORMATION: S at position 46 is a g or c
154 <400> SEQUENCE: 11
155 caacggcatc gcctaataaa cggccgctta attaagaagg aggtastaaa tatgaccgac 60
157 atcg 64
160 <210> SEQ ID NO: 12
161 <211> LENGTH: 46
162 <212> TYPE: DNA
163 <213> ORGANISM: Artificial
165 <220> FEATURE:
166 <223> OTHER INFORMATION: PCR primer
168 <400> SEQUENCE: 12
169 ttcgttttat ttgatgcctc tagattagtc cttgccgcgg tagagc 46
172 <210> SEQ ID NO: 13
173 <211> LENGTH: 20
174 <212> TYPE: DNA
175 <213> ORGANISM: Artificial
177 <220> FEATURE:
178 <223> OTHER INFORMATION: PCR primer
180 <400> SEQUENCE: 13
181 gagcaatcac ctatgaactg 20
184 <210> SEQ ID NO: 14
185 <211> LENGTH: 75
186 <212> TYPE: DNA
187 <213> ORGANISM: Artificial
189 <220> FEATURE:
190 <223> OTHER INFORMATION: PCR primer
192 <400> SEQUENCE: 14
193 gagcggctgg ttcatttgta ccttctctct ctttaatggc ggccgcacca ttcgcatggt 60
195 tttatgaaga atccc 75
198 <210> SEQ ID NO: 15
199 <211> LENGTH: 47
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial
203 <220> FEATURE:
204 <223> OTHER INFORMATION: PCR primer
206 <400> SEQUENCE: 15
207 cacacagaat gcggccgcga ggagaaaggt aaatatgaac atgccccg 47
210 <210> SEQ ID NO: 16
211 <211> LENGTH: 20
212 <212> TYPE: DNA

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213 <213> ORGANISM: Artificial
215 <220> FEATURE:
216 <223> OTHER INFORMATION: PCR primer
218 <400> SEQUENCE: 16
219 cgttcaccga caaacaacag                                20
222 <210> SEQ ID NO: 17
223 <211> LENGTH: 1347
224 <212> TYPE: DNA
225 <213> ORGANISM: Pseudomonas putida
228 <220> FEATURE:
229 <221> NAME/KEY: CDS
230 <222> LOCATION: (1)..(1344)
232 <400> SEQUENCE: 17
233 atg aac atg ccc gaa act ggt cct gcc ggt atc gcc agc cag ctc aag      48
234 Met Asn Met Pro Glu Thr Gly Pro Ala Gly Ile Ala Ser Gln Leu Lys
235 1                               5                               10                               15
237 ctg gac gcc cac tgg atg ccc tac acc gcc aac cgc aac ttc cag cgc      96
238 Leu Asp Ala His Trp Met Pro Tyr Thr Ala Asn Arg Asn Phe Gln Arg
239                               20                               25                               30
241 gac cca cgc ctg atc gtg gcg gcc gaa ggc aac tac ctg gtc gat gac      144
242 Asp Pro Arg Leu Ile Val Ala Ala Glu Gly Asn Tyr Leu Val Asp Asp
243                               35                               40                               45
245 cac ggg cgc aag atc ttc gac gcc ctg tcc ggc ctg tgg acc tgc ggc      192
246 His Gly Arg Lys Ile Phe Asp Ala Leu Ser Gly Leu Trp Thr Cys Gly
247                               50                               55                               60
249 gca ggg cac act cgc aag gaa atc gct gac gcg gtg acc cgt caa ctg      240
250 Ala Gly His Thr Arg Lys Glu Ile Ala Asp Ala Val Thr Arg Gln Leu
251 65                               70                               75                               80
253 agt acg ctg gac tac tcc cca gcg ttc cag ttc ggc cac ccg ctg tcg      288
254 Ser Thr Leu Asp Tyr Ser Pro Ala Phe Gln Phe Gly His Pro Leu Ser
255                               85                               90                               95
257 ttc cag ctg gcg gaa aag atc gcc gag ctg gtt ccg ggc aat ctg aat      336
258 Phe Gln Leu Ala Glu Lys Ile Ala Glu Leu Val Pro Gly Asn Leu Asn
259                               100                              105                              110
261 cac gtc ttc tat acc aac tcc ggt tcc gag tgc gcc gat acc gca ctg      384
262 His Val Phe Tyr Thr Asn Ser Gly Ser Glu Cys Ala Asp Thr Ala Leu
263                               115                              120                              125
265 aag atg gtg cgt gcc tac tgg cgc ctg aaa ggc cag gca acc aag acc      432
266 Lys Met Val Arg Ala Tyr Trp Arg Leu Lys Gly Gln Ala Thr Lys Thr
267                               130                              135                              140
269 aag atc atc ggc cgt gcc cgt ggt tac cat ggc gtg aac atc gcc ggt      480
270 Lys Ile Ile Gly Arg Ala Arg Gly Tyr His Gly Val Asn Ile Ala Gly
271 145                              150                              155                              160
273 acc agc ctg ggt ggc gtc aac ggt aac cgc aag atg ttt ggc cag ctg      528
274 Thr Ser Leu Gly Gly Val Asn Gly Asn Arg Lys Met Phe Gly Gln Leu
275                               165                              170                              175
277 ctg gac gtc gac cac ctg cct cac act gta ttg ccg gtg aac gcc ttc      576
278 Leu Asp Val Asp His Leu Pro His Thr Val Leu Pro Val Asn Ala Phe
279                               180                              185                              190

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281	tcg	aaa	ggc	ttg	ccg	gaa	gag	ggc	ggt	atc	gcg	ctg	gct	gac	gaa	atg	624
282	Ser	Lys	Gly	Leu	Pro	Glu	Glu	Gly	Gly	Ile	Ala	Leu	Ala	Asp	Glu	Met	
283			195						200					205			
285	ctc	aag	ctg	atc	gag	ctg	cac	gat	gcc	tcc	aac	atc	gca	gca	gtc	atc	672
286	Leu	Lys	Leu	Ile	Glu	Leu	His	Asp	Ala	Ser	Asn	Ile	Ala	Ala	Val	Ile	
287		210					215					220					
289	gtc	gag	ccg	ctg	gca	ggt	tcg	gcc	ggt	gtg	ctg	ccg	ccg	cca	aag	ggt	720
290	Val	Glu	Pro	Leu	Ala	Gly	Ser	Ala	Gly	Val	Leu	Pro	Pro	Pro	Lys	Gly	
291	225					230					235				240		
293	tac	ctg	aag	cgc	ctg	cgt	gaa	atc	tgc	acc	cag	cac	aac	att	ctg	ctg	768
294	Tyr	Leu	Lys	Arg	Leu	Arg	Glu	Ile	Cys	Thr	Gln	His	Asn	Ile	Leu	Leu	
295					245					250				255			
297	atc	ttc	gac	gaa	gtg	atc	aca	ggc	ttc	ggc	cgc	atg	ggc	gcg	atg	acc	816
298	Ile	Phe	Asp	Glu	Val	Ile	Thr	Gly	Phe	Gly	Arg	Met	Gly	Ala	Met	Thr	
299			260					265					270				
301	ggc	tcg	gaa	gcc	ttc	ggc	gtt	acc	ccg	gac	ctg	atg	tgc	atc	gcc	aag	864
302	Gly	Ser	Glu	Ala	Phe	Gly	Val	Thr	Pro	Asp	Leu	Met	Cys	Ile	Ala	Lys	
303			275					280					285				
305	cag	gtg	acc	aac	ggc	gcc	atc	ccg	atg	ggc	gca	gtg	att	gcc	agc	agc	912
306	Gln	Val	Thr	Asn	Gly	Ala	Ile	Pro	Met	Gly	Ala	Val	Ile	Ala	Ser	Ser	
307		290					295					300					
309	gag	atc	tac	cag	acc	ttc	atg	aac	cag	ccg	acc	ccg	gaa	tac	gcc	gtg	960
310	Glu	Ile	Tyr	Gln	Thr	Phe	Met	Asn	Gln	Pro	Thr	Pro	Glu	Tyr	Ala	Val	
311	305					310				315					320		
313	gaa	ttc	cca	cac	ggc	tac	acc	tat	tcg	gcg	cac	ccg	gta	gcc	tgt	gcc	1008
314	Glu	Phe	Pro	His	Gly	Tyr	Thr	Tyr	Ser	Ala	His	Pro	Val	Ala	Cys	Ala	
315					325					330				335			
317	gcc	ggt	ctc	gcc	gcg	ctg	gac	ctg	ctg	cag	aag	gaa	aac	ctg	gtg	cag	1056
318	Ala	Gly	Leu	Ala	Ala	Leu	Asp	Leu	Leu	Gln	Lys	Glu	Asn	Leu	Val	Gln	
319			340					345					350				
321	tcc	gcg	gct	gaa	ctg	gcg	ccg	cat	ttc	gag	aag	ctg	ctg	cac	ggc	gtg	1104
322	Ser	Ala	Ala	Glu	Leu	Ala	Pro	His	Phe	Glu	Lys	Leu	Leu	His	Gly	Val	
323			355					360					365				
325	aag	ggc	acc	aag	aat	atc	gtc	gat	atc	cgc	aac	tac	ggc	ctg	gcc	ggc	1152
326	Lys	Gly	Thr	Lys	Asn	Ile	Val	Asp	Ile	Arg	Asn	Tyr	Gly	Leu	Ala	Gly	
327		370					375					380					
329	gcc	atc	cag	atc	gcc	gcc	cgt	gac	ggt	gat	gcc	atc	ggt	cgc	cct	tac	1200
330	Ala	Ile	Gln	Ile	Ala	Ala	Arg	Asp	Gly	Asp	Ala	Ile	Val	Arg	Pro	Tyr	
331	385					390						395			400		
333	gaa	gcg	gcc	atg	aag	ctg	tgg	aaa	gcg	ggc	ttc	tat	gta	cgc	ttt	ggt	1248
334	Glu	Ala	Ala	Met	Lys	Leu	Trp	Lys	Ala	Gly	Phe	Tyr	Val	Arg	Phe	Gly	
335			405							410				415			
337	ggc	gac	acc	ctg	cag	ttc	ggc	cca	acc	ttc	aat	acc	aag	ccg	cag	gaa	1296
338	Gly	Asp	Thr	Leu	Gln	Phe	Gly	Pro	Thr	Phe	Asn	Thr	Lys	Pro	Gln	Glu	
339			420						425				430				
341	ctg	gac	cgc	ttg	ttc	gat	gct	ggt	ggc	gaa	acc	ctg	aac	ctg	atc	gac	1344
342	Leu	Asp	Arg	Leu	Phe	Asp	Ala	Val	Gly	Glu	Thr	Leu	Asn	Leu	Ile	Asp	
343			435					440					445				
345	tga																1347

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/581,570

DATE: 06/14/2006
TIME: 10:12:08

Input Set : A:\seq listing.app
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16

VERIFICATION SUMMARY

DATE: 06/14/2006

PATENT APPLICATION: US/10/581,570

TIME: 10:12:08

Input Set : A:\seq listing.app

Output Set: N:\CRF4\06142006\J581570.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date